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## NEMATODE H- LIKE SEQUENCES

1  
caa gtt tga gat att taa att att att ttg gtg cta aga aaa att ttg tga aaa ATG AAT  
M N

61  
TAT TCA AAG GAT GCC CCA GAA TTT GTT GTG TCT CCA AAA GAT GCA CGC GAA TTT GTT GTA  
Y S K D A P E F V V S P K D A R E F V V

121  
AAA TGT ATG CAA ACA GTT GGA ACA TCC CCT GAC CAT GCT GGT CAA TTA GCA GAT CTA TTA  
K C M Q T V G T S P D H A G Q L A D L L

181  
TTG GAT GCT GAT CTT GTT GGA CAC TAT AGT CAT GGT CTA AAT CGA CTT CAT ATT TAT GTG  
L D A D L V G H Y S H G L N R L H I Y V

241  
GAT GAC GTC AAA AAC GGA GTT AAA GGA AAT GGA GTT CCA AAA GTG TTA AAA CAA AAA GGA  
D D V K N G V K G N G V P K V L K Q K G

301  
GGC ACT GCT TGG GTT GAT GGA GAA AAT CTT CTG GGT GCA GTT GTT GGA AAC TTC TGT ACC  
G T A W V D G E N L L G A V V G N F C T

361  
GAC TTG GCT ATT AAA TTG GCT AAA GAA TTT GGC GTT GCT TGG GTG GTA ACA AAA AAT TCT  
D L A I K L A K E F G V A W V V T K N S

421  
AAT CAT TAT GGA GCT TGT CAA CAT TAT ACT AAG AAA ATT GCA AAT GCA GGA ATG GTG GGA  
N H Y G A C Q H Y T K K I A N A G M V G

481  
ATG TCT TTT ACA AAT ACA TCG CCT CTC ATG TTC CCC TGC CGA TCT TCT GAG ATT GGA CTT  
M S F T N T S P L M F P C R S S E I G L

541  
GGT ACA AAC CCT CTT TCT TGT TGT GTC AAC TCG GAA AAG ACA GGA GAC AGT TTT TTG TTA  
G T N P L S C C V N S E K T G D S F L L

601  
GAC ATG GCT ACG ACA ACT GTT GCT CTT GGA AAG GTA GAG CTG GCA GAT TGT CGC GGT AAA  
D M A T T T V A L G K V E L A D C R G K

661  
ACA CAA ATT CCC TCC ACA TGG GGT GCC GAT TCT AAA GGC AAT CCA TCG ACT GAT ACA CAA  
T Q I P S T W G A D S K G N P S T D T Q

721  
GTT GTT TTA CAC GGT GGC GGA CTT TTG CCT TTA GGC GGT ATA GAA GAG ACG GGA TCT TAC  
V V L H G G G L L P L G G I E E T G S Y

781  
AAA GGA ACG GGT CTT TCA ATG ATG GGT GAA TTG TTT TGT GGA ATT TTG GCA GGG TCA AGT  
K G T G L S M M G E L F C G I L A G S S

841  
TTT GGA AAA AAT GTA CGA TTA TGG GGG CAA TCA CAC AAA GCC GCT GAC AAT GGC CAA TGT  
F G K N V R L W G Q S H K A A D N G Q C

901  
TTT GTT GCT ATT GAT CAA GAA TGT TTT GCC CCA GGA TTT GCT CCT CGT TTA CAA CAA TTT  
F V A I D Q E C F A P G F A P R L Q Q F

961  
TTG GAT GAA ACA CGG AAT TTG AAA CCG ATT TCT GAA GAA AAG CCT GTT CTA GTG CCT GGA  
L D E T R N L K P I S E E K P V L V P G

1021  
GAT CCT GAA AGA ATG AAT ACA GAA TAT AGC CAA AAG GCT GGA GGT TTG GTA TAC CAA GAA  
D P E R M N T E Y S Q K A G G L V Y Q E

1081  
GGG CAG ATA AAA GCT TTG GAA GAG TTG GCC ACA AAA TGT GAT GTT CAA ATG TTC TCA TAC  
G Q I K A L E E L A T K C D V Q M F S Y

1141  
AAA CGA CTA AAA tga gga tga gat tta aat att ttt ttg tgt agc tga aac tga ctt caa  
K R L K \*

1201  
acg aga aat gaa caa ttt cct aaa aag cag tta gat aag ggt tta ttt ttc att tat tta

1261  
ttt ttt aac ctc att ttt tat ata cga ata aaa tta atg ctc \*aa aaa aaa aaa aaa

1321  
aaa aaa a

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FIGURE 1

1  
tgg tgc taa gaa aaa ttt tgt gcg aaa ATG AAT TAT TCA AAG GAT GCC CCA GAA TTT GTT  
M N Y S K D A P E F V  
61  
GTC TCT CCA AAA GAT GCT CGC GAA TTT GTT GTA AAA TGT ATG CAA ACA GTT GGA ACA TCC  
V S P K D A R E F V V K C M Q T V G T S  
121  
CCT GAC CAT GCT GGT CAA TTA GCA GAT CTC TTA TTA GAT GCT GAT CTT GTT GGG CAT TAC  
P D H A G Q L A D L L L D A D L V G H Y  
181  
AGT CAT GGT CTA AAT CGG CTT CAT ATT TAT GTG GAT GAC GTC AAA AAT GGA GTT AAA GGA  
S H G L N R L H I Y V D D V K N G V K G  
241  
AAT GGA GTT CCA AAA GTG TTA AAA CAA AAA GGA GGC ACT GCT TGG GTG GAT GGA GAA AAT  
N G V P K V L K Q K G G T A W V D G E N  
301  
CTT TTG GGT GCA GTT GTT GGC AAC TTC TGT ACC GAT TTG GCT ATT AAA TTG GCT AAA GAA  
L L G A V V G N F C T D L A I K L A K E  
361  
TTT GGT GTT GCT TGG GTG GTA ACA AAA AAT TCT AAT CAT TAT GGA GCT \*GT CAA CAT TAT  
F G V A W V V T K N S N H Y G A X Q H Y  
421  
ACT AAG AAA ATT GCG AAT GCA GGA ATG GTG GGA ATG TCA TTT ACA AAT ACT TCA CTT CTC  
T K K I A N A G M V G M S F T N T S P L  
481  
ATG TTC CCC TGC CGT TCT TCT GAG ATC GGA CTA GGC ACA AAC CCT CTT TCT TGT TGT GCC  
M F P C R S S E I G L G T N P L S C C A  
541  
AAC TCG GAA AAG ACA GAA GAC AGT TTT TTG TTA GAC ATG GCT ACT ACA ACT GTT GCT CTA  
N S E K T E D S F L L D M A T T T V A L  
601  
GGA AAG GTT GAG CTG GCA AAT TGT CGC GGT AAA ACA CAA ATT CCC TCA GCA TGG GGT GCC  
G K V E L A N C R G K T Q I P S A W G A  
661  
GAT TCT AAA GGC AAT CCA TCA ACA GAC ACA CAA GTT GTT TTA CAT GGT GGC GGA CTT TTG  
D S K G N P S T D T Q V V L H G G G L L  
721  
CCT TTA GGC GGT ATA GAA GAG ACG GGA TCT TAC AAA GGA ACG GGT CTC TCA ATG ATG GGT  
P L G G I E E T G S Y K G T G L S M M G  
781  
GAA TTG TTT TGT GGA ATT TTG GCA GGG TCA AGT TTT GGA AAA AAT GTA CGA TTA TGG GGG  
E L F C G I L A G S S F G K N V R L W G  
841  
CAA TCA CAC AAA GCC GCT GAC AAT GGC CAA TGT TTT GTT GCT ATT GAT CAA GAA TGT TTT  
Q S H K A A D N G Q C F V A I D Q E C F  
901  
GCC CCA GGA TTT GCT CCT CGT TTA CAA CAA TTT TTG GAT GAA ACA CGG AAT TTG AAA CCG  
A P G F A P R L Q Q F L D E T R N L K P  
961  
ATT TCT GAA GAA AAG CCT GTT CTA GTG CCT GGA GAT CCT GAA AGA ATG AAT ACA GAA TAT  
I S E E K P V L V P G D P E R M N T E Y  
1021  
AGC CAA AAG GCT GGA GGT TTG GTA TAC CAA GAA GGG CAG ATA AAA GCT TTG GAA GAG TTG  
S Q K A G G L V Y Q E G Q I K A L E E L  
1081  
GCC ACA AAA TGT GAT GTT CAA ATG TTC TCA TAC AAA CGA CTA AAA TGA gga tga gat tta  
A T K C D V Q M F S Y K R L K \*  
1141  
aat att ttt ttg tgt agc tga aac tga ctt caa acg aga aat gaa caa ttt cct aaa aag  
1201  
cag tta gat aag ggt tta ttt ttc att tat tta ttt ttt aac ctc att ttt tat ata cga  
1261  
agc aga tat gac tga aac tgg agg tgg tga ttc tgt tga atc tgc aag tgt tta tgc taa

FIGURE 2A

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132.  
ctc tgt ttg tga aat gtg cgg aaa tta tga ggt tca act tca aac aat tca aag cag tca

1381  
gga tac tct cag gga gaa att ggc agc tgc taa aga att gta tga gaa ata tgg caa gga

1441  
att gac aga aga gag gca tta tgc aaa gga att gga aat taa att tgc tgc ttt aaa tga

1501  
aga aac tga agg gaa aat tca gca atg tat tac caa tac aga aga ctt tga cag cgt att

1561  
gcc ttc tca gta aaa aac aa\* aag ctg att tgt ctg ttt tgg aat c\*c aat tag aat tgg

1621  
cta gga atc gtc aaa aag agc ttc aag aac aat tgg ttt tgt taa atg aaa ggt atg aaa

1681  
aac ttt tac att taa aat ctc aat gtg ctg aag aaa tgc gtg aac aac aaa ttg aac tgc

1721  
ctc aaa cag ttg aag aac ttc aat ttt tgg cat tgc agt tga \*ag agg aat tga taa ctg

1781  
aac gtg cag cac gtg agc atg aaa gga ggg aat taa atg atg aat tgg cta tgg cac gtc

1841  
aac agc ttg ttg aat tgg aaa ttt gtc c\*a gag aaa atg aag aat gaa ttt tat gat ata

1901  
taa aaa tat att tat ttt gct caa ata g\*t ttt ata aat ttt aag agc tga tag aaa aat

1961  
tta gtt ttg \*aa ttt ttg aag aat ata ttt t\*t acg gtt tgc ac\* cct tag aat ggt ttt

2021  
gtt tta ata aat gc\* c\*g gtt gg\* aaa aaa aaa aaa aaa aaa aaa

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# Amino acid alignment

1 *M. incognita* MDH1

2 *M. incognita* MDH2

3 *C. elegans* MDH1

4 *C. elegans* MDH2

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      10      20      30      40      50      60
1  .....MNYSDAPFVVSPKDAREFVVK: 23
2  .....MNYSDAPFVVSPKDAREFVVK: 23
3  .....MTIKDKREFNETDEIVISKEKLDSEVLE: 28
4  MNLLQRALVFTGGHISRYQAVIAVNSVGKNARYSTTDDNMAAPEESVVAKDEMKRIMVE: 60

      70      80      90     100     110     120
1  CMQTVGTSPDHAGQLADLLDADLVGHYSHGLNRLHIYVDDVKNG VKGNGVPEKVLKQKG: 82
2  CMQTVGTSPDHAGQLADLLDADLVGHYSHGLNRLHIYVDDVKNG VKGNGVPEKVLKQKG: 82
3  CLAKAGCTGDHAQQLAETLLCSDFRGHYSHGILNRLHIYVDDLMKSTAVTGTTPQVLKSKG: 88
4  CMTKVGATESHATQLALVLLGDIRGHYSHGLNRLDMYVRDIEQNVCKGDGEPILKEKA:120

     130     140     150     160     170     180
1  GTAWVDGEMLLGAVVGHTFCTDLAIKLAKKEFGVAVVVTKNSHHYGACQHYTKKIANAGMVG:142
2  GTAWVDGEMLLGAVVGHTFCTDLAIKLAKKEFGVAVVVTKNSHHYGACQHYTKKIANAGMVG:142
3  STAWVDGEMLLGAVVGHTFCTDLAVEKAKEFGIGVWVVCRESHHFGIAGWYADFACRNLVVG:148
4  GTAWVDGEMLLGAVVGHTFCTDLAIEKAKNAGIGVWVAKGSHHYGTAGWYALRAMKKGMIG:180

     190     200     210     220     230     240
1  MSFTNTSPIMFPCRSSEIGLGTNPSCCVNSEKTGDSFLLDMATTTVALGKVELADCRGK:202
2  MSFTNTSPIMFPCRSSEIGLGTNPSCCANSEKTGDSFLLDMATTTVALGKVELADCRGK:202
3  MATNTNTSPCVFPTGSEKSLGSPNPI.CMAAPGMEGDSFLLDMASTTVAYGKIEVVDRKGE:207
4  MSMTHNTSPISFPTRSAPVALGTNPI.SLAAPGTGDDSFVLDMASTTVAILGKVELAARK.E:238

     250     260     270     280     290     300
1  TQIPSTWGADSKGNPSNTDTQVVLHGGGLLPGLGIEETGSEYKGTGLSMMGELFCGILAGSS:262
2  TQIPSAWGADSKGNPSNTDTQVVLHGGGLLPGLGIEETGSEYKGTGLSMMGELFCGILAGSS:262
3  TYIPGSWGADKNGDETHNPKEVLDGGGLQPLGGESEITGGYKGTGLCMMVEVLCCGIMGCSA:267
4  NPVPLSWGVGEGGKETDTPTRKVLVYGGGLLPGLGVEVSGGYKGVGLSSMIETFCGILAGAH:298

     310     320     330     340     350     360
1  FGKENVRLWGQSHKAADNGQCFVAIDQECFAPGFAPRLQQLDETRELKPISEEEKPVILVPG:322
2  FGKENVRLWGQSHKAADNGQCFVAIDQECFAPGFAPRLQQLDETRELKPISEEEKPVILVPG:322
3  FGKENVRLWGQSHKAADNGQCFVAIDQECFAPGFAPRLQQLDETRELKPISEEEKPVILVPG:322
4  WGPVVRKVMSTKSEADNGQCFVAIDPEAFAPGFADRLQDEMOTMRALETSSPSFKVEVAG:358

     370     380     390     400
1  DPERMNTTEYSQKAGGLVYQEGQIKALEELATKCDVQMISYKRLK.:366
2  DPERMNTTEYSQKAGGLVYQEGQIKALEELATKCDVQMISYKRLK.:366
3  DPERAHNMCDLGGIVYKKKQLDHLKNLADRLGVIMRLVDEKPG:372
4  DMERRHEALVEQLGGIPYHKNQITTFVNDLAAKLGVKTVDLVQ....:400

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FIGURE 3

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